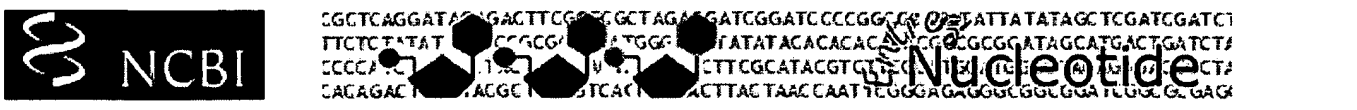
09/509,775



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***603480** Links

PROTEASOME 26S SUBUNIT, NON-ATPase, 10; PSMD10

Alternative titles; symbols

p28

TEXT

Ubiquitinated proteins are degraded by a 26S ATP-dependent protease. The protease is composed of a 20S catalytic proteasome and PA700, a 700-kD regulatory complex (see PSMC1, 602706). Hori et al. (1998) determined the partial protein sequences of bovine p28 and p40.5 (PSMD13; 603481), 2 components of PA700. By searching a sequence database, they identified cDNAs encoding the human p28 and p40.5 homologs. The predicted 226-amino acid human p28 protein contains 5 ankyrin repeats, which are thought to function in protein-protein interactions. Using computerized homology searches, Hori et al. (1998) identified Nas6, an S. cerevisiae gene encoding a protein with 38% identity to p28. They found that disruption of Nas6 had no effect on cell viability. Northern blot analysis revealed that p28 was expressed as a 1.3-kb mRNA in all human tissues tested.

REFERENCES

1. Hori, T.; Kato, S.; Saeki, M.; DeMartino, G. N.; Slaughter, C. A.; Takeuchi, J.; Toh-e, A.; Tanaka, K. :
cDNA cloning and functional analysis of p28 (Nas6p) and p40.5 (Nas7p), two novel regulatory subunits of the 26S proteasome. *Gene* 216: 113-122, 1998.
PubMed ID : 9714768

CREATION DATE

Rebekah S. Rasooly : 2/3/1999

EDIT HISTORY

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1: Gene 1998 Aug 17;216(1):113-22

cDNA cloning and functional analysis of p28 (Nas6p) and p40.5 (Nas7p), two novel regulatory subunits of the 26S proteasome.

Hori T, Kato S, Saeki M, DeMartino GN, Slaughter CA, Takeuchi J, Toh-e A, Tanaka K.

The Tokyo Metropolitan Institute of Medical Science, and CREST, Japan Science and Technology Corporation (JST), 3-18-22 Honkomagome, Bunkyo-ku, Tokyo 113-8613, Japan.

We employed cDNA cloning to deduce the complete primary structures of p28 and p40.5, two novel subunits of PA700 (also called 19S complex), a 700 kDa multisubunit regulatory complex of the human 26S proteasome. These polypeptides consisted of 226 and 376 amino acids with calculated molecular masses of 24428 Da and 42945 Da, and isoelectric points of 5.68 and 5.46, respectively. Intriguingly, p28 contained five conserved motifs known as 'ankyrin repeats', implying that this subunit may contribute to interaction of the 26S proteasome with other protein(s). Computer-assisted homology analysis revealed high sequence similarities of p28 and p40.5 with yeast proteins, termed Nas6p and Nas7p (non-ATPase subunits 6 and 7), respectively, whose functions are as yet unknown. Disruption of these yeast genes, NAS6 and NAS7, had no effect on cell viability, indicating that neither of the two subunits is essential for proliferation of yeast cells. However, the NAS7, but not NAS6, disruptant cells caused high sensitivity to heat stress, being unable to proliferate at 37 degreesC.

PMID: 9714768 [PubMed - indexed for MEDLINE]